



## SEQUENCE LISTING

<110> Zankel et al.

<120> MEGALIN-BASED DELIVERY OF THERAPEUTIC COMPOUNDS TO THE BRAIN AND OTHER TISSUES

<130> 31075/40037

<140> 10/812,849

<141> 2004-03-30

<150> US 10/600,862

<151> 2003-06-20

<160> 29

<170> PatentIn version 3.2

<210> 1

<211> 323

<212> PRT

<213> Homo sapiens

<400> 1

Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg Glu Ser  
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Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu Lys Ala  
20 25 30

Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His Ala Asp  
35 40 45

Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu Lys Leu  
50 55 60

Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile Arg Asn  
65 70 75 80

Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys Asp Ala  
85 90 95

Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp Gly Leu  
100 105 110

Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly  
115 120 125

Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His  
130 135 140

His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser  
145 150 155 160

Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser  
165 170 175

Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu  
180 185 190

Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser  
195 200 205

His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile  
210 215 220

Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu  
225 230 235 240

Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys  
245 250 255

His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg  
260 265 270

His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu  
275 280 285

Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val  
290 295 300

Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His  
305 310 315 320

Asn Glu Leu

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<213> Homo sapiens

<400> 2

Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly Lys Phe  
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Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His His Lys  
20 25 30

Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser Arg Thr

35

40

45

Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser Asp Ile  
50 55 60

Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu Lys Leu  
65 70 75 80

Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser His Gln  
85 90 95

Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile Asp Leu  
100 105 110

Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu Glu Ala  
115 120 125

Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn  
130 135 140

His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg His Ala  
145 150 155 160

Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu Lys His  
165 170 175

Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val Lys Lys  
180 185 190

His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His Asn Glu  
195 200 205

Leu

<210> 3  
<211> 33  
<212> DNA  
<213> Artificial sequence

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<223> Synthetic primer

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Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly Ile Ser  
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Val Arg Leu Thr Ser Cys Ala Arg Val Leu His Tyr Lys Glu Lys Ile  
 20 25 30

His Glu Tyr Asn Val Leu Leu Asp Thr Leu Ser Arg Ala Glu Glu Gly  
 35 40 45

Tyr Glu Asn Leu Leu Ser Pro Ser Asp Met Thr His Ile Lys Ser Asp  
 50 55 60

Thr Leu Ala Ser Lys His Ser Glu Leu Lys Asp Arg Leu Arg Ser Ile  
 65 70 75 80

Asn Gln Gly Leu Asp Arg Leu Arg Lys Val Ser His Gln Leu Arg Pro  
 85 90 95

Ala Thr Glu Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Leu Ala  
 100 105 110

Gln Ser Ala Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu  
 115 120 125

Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn His Tyr Gln Lys  
 130 135 140

Gln Leu Glu Ile Ser His Gln Lys Leu Lys His Val Glu Ser Ile Gly  
 145 150 155 160

Asp Pro Glu His Ile Ser Arg Asn Lys Glu Lys Tyr Val Leu Leu Glu  
 165 170 175

Glu Lys Thr Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp  
 180 185 190

Leu Ser Ser Arg Val Ser Arg Ala Arg His Asn Glu Leu

195

200

205

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cctgtctcca acttcaccta cagccccac accaagggtcc tggacatctg tgtctcgctg 3660  
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<211> 1228  
<212> PRT  
<213> Artificial sequence

<220>  
<223> RAP-GAA fusion sequence

<400> 7

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Val Leu Gly Ser Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro  
20 25 30

Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu  
35 40 45

Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu  
50 55 60

Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys  
65 70 75 80

Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg  
85 90 95

Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly  
100 105 110

Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln  
115 120 125

Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala  
130 135 140

Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg  
145 150 155 160

Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu  
165 170 175

Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro  
180 185 190

Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr  
195 200 205

Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu  
210 215 220

Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu  
225 230 235 240

Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr  
245 250 255

Asp Lys Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala  
260 265 270

Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His  
275 280 285

Glu Lys Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser  
290 295 300

Arg Ser Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu  
305 310 315 320

Gly Tyr Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser  
325 330 335

Arg Ala Arg Ala Glu Ala Glu Thr Gly Ala His Pro Gly Arg Pro Arg  
340 345 350

Ala Val Pro Thr Gln Cys Asp Val Pro Pro Asn Ser Arg Phe Asp Cys  
355 360 365

Ala Pro Asp Lys Ala Ile Thr Gln Glu Gln Cys Glu Ala Arg Gly Cys  
370 375 380

Cys Tyr Ile Pro Ala Lys Gln Gly Leu Gln Gly Ala Gln Met Gly Gln  
385 390 395 400

Pro Trp Cys Phe Phe Pro Pro Ser Tyr Pro Ser Tyr Lys Leu Glu Asn  
405 410 415

Leu Ser Ser Ser Glu Met Gly Tyr Thr Ala Thr Leu Thr Arg Thr Thr  
420 425 430

Pro Thr Phe Phe Pro Lys Asp Ile Leu Thr Leu Arg Leu Asp Val Met  
435 440 445

Met Glu Thr Glu Asn Arg Leu His Phe Thr Ile Lys Asp Pro Ala Asn  
450 455 460

Arg Arg Tyr Glu Val Pro Leu Glu Thr Pro Arg Val His Ser Arg Ala  
465 470 475 480

Pro Ser Pro Leu Tyr Ser Val Glu Phe Ser Glu Glu Pro Phe Gly Val  
485 490 495

Ile Val His Arg Gln Leu Asp Gly Arg Val Leu Leu Asn Thr Thr Val  
500 505 510

Ala Pro Leu Phe Phe Ala Asp Gln Phe Leu Gln Leu Ser Thr Ser Leu  
515 520 525

Pro Ser Gln Tyr Ile Thr Gly Leu Ala Glu His Leu Ser Pro Leu Met  
530 535 540

Leu Ser Thr Ser Trp Thr Arg Ile Thr Leu Trp Asn Arg Asp Leu Ala  
545 550 555 560

Pro Thr Pro Gly Ala Asn Leu Tyr Gly Ser His Pro Phe Tyr Leu Ala  
565 570 575

Leu Glu Asp Gly Gly Ser Ala His Gly Val Phe Leu Leu Asn Ser Asn  
580 585 590

Ala Met Asp Val Val Leu Gln Pro Ser Pro Ala Leu Ser Trp Arg Ser  
595 600 605

Thr Gly Gly Ile Leu Asp Val Tyr Ile Phe Leu Gly Pro Glu Pro Lys  
610 615 620

Ser Val Val Gln Gln Tyr Leu Asp Val Val Gly Tyr Pro Phe Met Pro  
625 630 635 640

Pro Tyr Trp Gly Leu Gly Phe His Leu Cys Arg Trp Gly Tyr Ser Ser  
645 650 655

Thr Ala Ile Thr Arg Gln Val Val Glu Asn Met Thr Arg Ala His Phe  
660 665 670

Pro Leu Asp Val Gln Trp Asn Asp Leu Asp Tyr Met Asp Ser Arg Arg  
675 680 685

Asp Phe Thr Phe Asn Lys Asp Gly Phe Arg Asp Phe Pro Ala Met Val  
690 695 700

Gln Glu Leu His Gln Gly Gly Arg Arg Tyr Met Met Ile Val Asp Pro  
705 710 715 720

Ala Ile Ser Ser Ser Gly Pro Ala Gly Ser Tyr Arg Pro Tyr Asp Glu  
725 730 735

Gly Leu Arg Arg Gly Val Phe Ile Thr Asn Glu Thr Gly Gln Pro Leu  
740 745 750

Ile Gly Lys Val Trp Pro Gly Ser Thr Ala Phe Pro Asp Phe Thr Asn  
755 760 765

Pro Thr Ala Leu Ala Trp Trp Glu Asp Met Val Ala Glu Phe His Asp  
770 775 780

Gln Val Pro Phe Asp Gly Leu Trp Ile Asp Met Asn Glu Pro Ser Asn  
785 790 795 800

Phe Ile Arg Gly Ser Glu Asp Gly Cys Pro Asn Asn Glu Leu Glu Asn  
805 810 815

Pro Pro Tyr Val Pro Gly Val Val Gly Gly Thr Leu Gln Ala Ala Thr  
820 825 830

Ile Cys Ala Ser Ser His Gln Phe Leu Ser Thr His Tyr Asn Leu His  
835 840 845

Asn Leu Tyr Gly Leu Thr Glu Ala Ile Ala Ser His Arg Ala Leu Val  
850 855 860

Lys Ala Arg Gly Thr Arg Pro Phe Val Ile Ser Arg Ser Thr Phe Ala  
865 870 875 880

Gly His Gly Arg Tyr Ala Gly His Trp Thr Gly Asp Val Trp Ser Ser  
885 890 895

Trp Glu Gln Leu Ala Ser Ser Val Pro Glu Ile Leu Gln Phe Asn Leu  
900 905 910

Leu Gly Val Pro Leu Val Gly Ala Asp Val Cys Gly Phe Leu Gly Asn  
915 920 925

Thr Ser Glu Glu Leu Cys Val Arg Trp Thr Gln Leu Gly Ala Phe Tyr  
930 935 940

Pro Phe Met Arg Asn His Asn Ser Leu Leu Ser Leu Pro Gln Glu Pro  
945 950 955 960

Tyr Ser Phe Ser Glu Pro Ala Gln Ala Met Arg Lys Ala Leu Thr  
965 970 975

Leu Arg Tyr Ala Leu Leu Pro His Leu Tyr Thr Leu Phe His Gln Ala  
980 985 990

His Val Ala Gly Glu Thr Val Ala Arg Pro Leu Phe Leu Glu Phe Pro  
995 1000 1005

Lys Asp Ser Ser Thr Trp Thr Val Asp His Gln Leu Leu Trp Gly  
1010 1015 1020

Glu Ala Leu Leu Ile Thr Pro Val Leu Gln Ala Gly Lys Ala Glu  
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Val Thr Gly Tyr Phe Pro Leu Gly Thr Trp Tyr Asp Leu Gln Thr  
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Val Pro Ile Glu Ala Leu Gly Ser Leu Pro Pro Pro Ala Ala  
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Pro Arg Glu Pro Ala Ile His Ser Glu Gly Gln Trp Val Thr Leu  
1070 1075 1080

Pro Ala Pro Leu Asp Thr Ile Asn Val His Leu Arg Ala Gly Tyr  
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Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr Thr Thr Glu Ser Arg  
1100 1105 1110

Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr Lys Gly Gly Glu  
1115 1120 1125

Ala Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser Leu Glu Val  
1130 1135 1140

Leu Glu Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala Arg Asn  
1145 1150 1155

Asn Thr Ile Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly Ala  
1160 1165 1170

Gly Leu Gln Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala  
1175 1180 1185

Pro Gln Gln Val Leu Ser Asn Gly Val Pro Val Ser Asn Phe Thr  
1190 1195 1200

Tyr Ser Pro Asp Thr Lys Val Leu Asp Ile Cys Val Ser Leu Leu  
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Met Gly Glu Gln Phe Leu Val Ser Trp Cys  
1220 1225

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<211> 2937  
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<223> RAP-IDU fusion sequence

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ttacccgccc gcggccgcct gaccctgcgc cccgcgcgtc ggctgcccgtc gctttgctg	2580
gtgcacgtgt gtgcgcgcggc cgagaagccg cccgggcagg tcacgcggct ccgcgcctg	2640
ccctgaccc aaggcgagct gttctggtc tggtcggatg aacacgtggg ctccaaagtgc	2700
ctgtggacat acgagatcca gttctctcag gacggtaagg cgtacacccc ggtcagcagg	2760
aagccatcga cttcaacact ctttgggttc agcccagaca caggtgctgt ctctggctcc	2820
taccgagttc gagccctgga ctactgggcc cgaccaggcc cttctcgga ccctgtgcgg	2880
tacctggagg tccctgtgcc aagagggccc ccattcccg gcaatccatg actcgag	2937

<210> 9  
 <211> 972  
 <212> PRT  
 <213> Artificial sequence  
  
 <220>

<223> RAP-IDU fusion sequence

<400> 9

Met Arg Gly Pro Ser Gly Ala Leu Trp Leu Leu Leu Ala Leu Arg Thr  
1 5 10 15

Val Leu Gly Ser Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro  
20 25 30

Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu  
35 40 45

Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu  
50 55 60

Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys  
65 70 75 80

Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg  
85 90 95

Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly  
100 105 110

Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln  
115 120 125

Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala  
130 135 140

Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg  
145 150 155 160

Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu  
165 170 175

Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro  
180 185 190

Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr  
195 200 205

Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu  
210 215 220

Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu  
225 230 235 240

Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr  
245 250 255

Asp Lys Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala  
260 265 270

Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His  
275 280 285

Glu Lys Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser  
290 295 300

Arg Ser Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu  
305 310 315 320

Gly Tyr Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser  
325 330 335

Arg Ala Arg Ala Glu Ala Glu Thr Gly Glu Ala Pro His Leu Val His  
340 345 350

Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser  
355 360 365

Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val  
370 375 380

Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val Pro  
385 390 395 400

His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu Val  
405 410 415

Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His  
420 425 430

Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly  
435 440 445

Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp  
450 455 460

Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg  
465 470 475 480

Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe  
485 490 495

Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser Met  
500 505 510

Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly Leu  
515 520 525

Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser Phe  
530 535 540

His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys  
545 550 555 560

His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp  
565 570 575

Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu  
580 585 590

Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys  
595 600 605

Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly  
610 615 620

Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met  
625 630 635 640

Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr  
645 650 655

Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu  
660 665 670

Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe  
675 680 685

Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro  
690 695 700

Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln Leu  
705 710 715 720

Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr  
725 730 735

Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp Ala  
740 745 750

Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His  
755 760 765

Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro  
770 775 780

Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys  
785 790 795 800

Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr  
805 810 815

Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala Ala  
820 825 830

Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro Ala  
835 840 845

Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu  
850 855 860

Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln  
865 870 875 880

Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys  
885 890 895

Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr  
900 905 910

Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro  
915 920 925

Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp Tyr  
930 935 940

Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val  
945 950 955 960

Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro  
965 970

<210> 10  
<211> 1398  
<212> DNA  
<213> Artificial sequence

<220>  
<223> RAP-GDNF fusion sequence

<400> 10  
 atgggggggtt cttactcgcg ggagaagaac cagcccaagc cgtccccgaa acgcgagtcc 60  
 ggagaggagt tccgcatttga gaagtttgaac cagctgtggg agaaggccca gcgactgcat 120  
 cttcctcccg tgaggctggc cgagctccac gctgatctga agatacagga gagggacgaa 180  
 ctcgccttggaa agaaactaaa gcttgcacggc ttggacgaag atggggagaa ggaagcgaga 240  
 ctcatacgca acctcaatgt catcttggcc aagtatggtc tggacggaaa gaaggacgct 300  
 cggcagggtga ccagcaactc cctcagtggc acccaggaag acgggcttggaa tgaccccagg 360  
 ctggaaaagc tgtggcacaa ggcgaagacc tctggaaat tctccggcga agaactggac 420  
 aagctctggc gggagttcct gcatcacaaa gagaagttt acgagtacaa cgtcctgctg 480  
 gagacccttga gcaggaccga agaaatccac gagaacgtca tttagcccttc ggacctgagc 540  
 gacatcaagg gcagcgtcct gcacagcagg cacacggagc tgaaggagaa gctgcgcagc 600  
 atcaaccagg gcctggaccg cctgcgcagg gtcagccacc agggctacag cactgaggt 660  
 gagttcgagg agcccagggt gattgacctg tggacctgg cgcaagtccgc caacctcact 720  
 gacaaggagc tggagggcggtt ccgggaggag ctcaagcact tcgaagccaa aatcgagaag 780  
 cacaaccact accagaagca gctggagatt ggcacgaga agctgaggca cgccagagagc 840  
 gtgggcacg gcgagcgtgt gagccgcagc cgcgagaagc acggccctgct ggagggcgg 900  
 accaaggagc tgggctacac ggtgaagaag catctgcagg acctgtccgg caggatctcc 960  
 agagctcggg ccgaggcaga aaccggttca ccagataaac aaatggcagt gcttcctaga 1020  
 agagagcggg atcggcaggc tgcagctgcc aaccagaga attccagagg aaaaggtcgg 1080  
 agaggccaga gggcaaaaaa ccggggttgt gtcttaactg caatacattt aaatgtcact 1140  
 gacttgggtc tgggctatga aaccaaggag gaactgattt ttaggtactg cagcggctct 1200  
 tgcgatgcag ctgagacaac gtacgacaaa atattgaaaa acttatccag aaatagaagg 1260  
 ctggtgagtg acaaagttagg gcaggcatgt tgcagaccca tcgccttga tgatgacctg 1320  
 tcgttttag atgataacct ggtttaccat attctaagaa agcattccgc taaaaggtgt 1380  
 ggatgtatct gatctaga 1398

<210> 11  
 <211> 463  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> RAP-GDNF fusion sequence

<400> 11

Met Gly Gly Ser Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro  
 1 5 10 15

Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu  
20 25 30

Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu  
35 40 45

Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys  
50 55 60

Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg  
65 70 75 80

Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly  
85 90 95

Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln  
100 105 110

Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala  
115 120 125

Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg  
130 135 140

Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu  
145 150 155 160

Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro  
165 170 175

Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr  
180 185 190

Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu  
195 200 205

Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu  
210 215 220

Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr  
225 230 235 240

Asp Lys Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala  
245 250 255

Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His  
260 265 270

Glu Lys Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser  
275 280 285

Arg Ser Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu  
290 295 300

Gly Tyr Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser  
305 310 315 320

Arg Ala Arg Ala Glu Ala Glu Thr Gly Ser Pro Asp Lys Gln Met Ala  
325 330 335

Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro  
340 345 350

Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg  
355 360 365

Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu  
370 375 380

Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser  
385 390 395 400

Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser  
405 410 415

Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg  
420 425 430

Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val  
435 440 445

Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile  
450 455 460

<210> 12  
<211> 49  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic primer

<400> 12  
gcgataggat cctactcgcg ggagaagaac cagcccaagc cgtccccga 49

<210> 13  
<211> 57  
<212> DNA

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<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 13
gcgataaaacc ggtttctgcc tcggcgcgag ctctggagat cctgccggac aggtcct 57

<210> 14
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 14
gcgataaccg gtgcacacacc cggccgtccc agagcagtg 39

<210> 15
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 15
gcgataactcg agtcaaacacc agctgacgag aaactgc 37

<210> 16
<211> 46
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 16
gcgataaccg gtgagggcccc ccgcacctgg tgcatgtgga cgcggc 46

<210> 17
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 17
gcgataactcg agtcatggat tgccccggga tggggggccct cttgg 45

<210> 18
<211> 33
<212> DNA
<213> Artificial sequence

<220>

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<223> Synthetic primer

<400> 18

acagtgaccg gttcaccaga taaacaaatg gca

33

<210> 19

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 19

acagtgctcg agtctagatc agatacatcc acaccttt

38

<210> 20

<211> 51

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 20

acagtggcca tgggggggttc ttactcgccg gagaagaacc agcccaagcc g

51

<210> 21

<211> 357

<212> PRT

<213> Homo sapiens

<400> 21

Met Ala Pro Arg Arg Val Arg Ser Phe Leu Arg Gly Leu Pro Ala Leu  
1 5 10 15

Leu Leu Leu Leu Leu Phe Leu Gly Pro Trp Pro Ala Ala Ser His Gly  
20 25 30

Gly Lys Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg  
35 40 45

Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu  
50 55 60

Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His  
65 70 75 80

Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu  
85 90 95

Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile  
100 105 110

Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys  
115 120 125

Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp  
130 135 140

Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr  
145 150 155 160

Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe  
165 170 175

Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr  
180 185 190

Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp  
195 200 205

Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu  
210 215 220

Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg  
225 230 235 240

Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg  
245 250 255

Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys  
260 265 270

Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile  
275 280 285

Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys  
290 295 300

Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser  
305 310 315 320

Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr  
325 330 335

Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala  
340 345 350

Arg His Asn Glu Leu  
355

<210> 22  
<211> 378  
<212> PRT  
<213> Mus musculus

<400> 22

Met Gly Gly Pro Thr Arg Pro Ser Pro Val Ser Leu Leu Ala Leu Gln  
1 5 10 15

Arg Lys Met Ala Pro Arg Arg Glu Arg Val Ser Thr Leu Pro Arg Leu  
20 25 30

Gln Leu Leu Val Leu Leu Leu Pro Leu Met Leu Val Pro Gln Pro  
35 40 45

Ile Ala Gly His Gly Gly Lys Tyr Ser Arg Glu Lys Asn Glu Pro Glu  
50 55 60

Met Ala Ala Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu  
65 70 75 80

Asn Gln Leu Trp Glu Lys Ala Lys Arg Leu His Leu Ser Pro Val Arg  
85 90 95

Leu Ala Glu Leu His Ser Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu  
100 105 110

Asn Trp Lys Lys Leu Lys Val Glu Gly Leu Asp Lys Asp Gly Glu Lys  
115 120 125

Glu Ala Lys Leu Ile His Asn Leu Asn Val Ile Leu Ala Arg Tyr Gly  
130 135 140

Leu Asp Gly Arg Lys Asp Ala Gln Met Val His Ser Asn Ala Leu Asn  
145 150 155 160

Glu Asp Thr Gln Asp Glu Leu Gly Asp Pro Arg Leu Glu Lys Leu Trp  
165 170 175

His Lys Ala Lys Thr Ser Gly Lys Phe Ser Ser Glu Glu Leu Asp Lys  
180 185 190

Leu Trp Arg Glu Phe Leu His Tyr Lys Glu Lys Ile Gln Glu Tyr Asn  
195 200 205

Val Leu Leu Asp Thr Leu Ser Arg Ala Glu Glu Gly Tyr Glu Asn Leu  
210 215 220

Leu Ser Pro Ser Asp Met Ala His Ile Lys Ser Asp Thr Leu Ile Ser  
225 230 235 240

Lys His Ser Glu Leu Lys Asp Arg Leu Arg Ser Ile Asn Gln Gly Leu  
245 250 255

Asp Arg Leu Arg Lys Val Ser His Gln Gly Tyr Gly Ser Thr Thr Glu  
260 265 270

Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala  
275 280 285

Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu Leu Lys His  
290 295 300

Phe Glu Ala Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu  
305 310 315 320

Ile Ser His Gln Lys Leu Lys His Val Glu Ser Ile Gly Asp Pro Glu  
325 330 335

His Ile Ser Arg Asn Lys Glu Lys Tyr Val Leu Leu Glu Glu Lys Thr  
340 345 350

Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp Leu Ser Ser  
355 360 365

Arg Val Ser Arg Ala Arg His Asn Glu Leu  
370 375

<210> 23  
<211> 357  
<212> PRT  
<213> Rat

<400> 23

Leu Arg Asp Arg Val Ser Thr Leu Pro Arg Leu Gln Leu Leu Val Leu  
1 5 10 15

Leu Leu Leu Pro Leu Leu Leu Val Pro Gln Pro Ile Ala Gly His Gly  
20 25 30

Gly Lys Tyr Ser Arg Glu Lys Asn Glu Pro Glu Met Ala Ala Lys Arg  
35 40 45

Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu  
50 55 60

Lys Ala Lys Arg Leu His Leu Ser Pro Val Arg Leu Ala Glu Leu His  
65 70 75 80

Ser Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Asn Trp Lys Lys Leu  
85 90 95

Lys Val Glu Gly Leu Asp Gly Asp Gly Glu Lys Glu Ala Lys Leu Val  
100 105 110

His Asn Leu Asn Val Ile Leu Ala Arg Tyr Gly Leu Asp Gly Arg Lys  
115 120 125

Asp Thr Gln Thr Val His Ser Asn Ala Leu Asn Glu Asp Thr Gln Asp  
130 135 140

Glu Leu Gly Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr  
145 150 155 160

Ser Gly Lys Phe Ser Ser Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe  
165 170 175

Leu His Tyr Lys Glu Lys Ile His Glu Tyr Asn Val Leu Leu Asp Thr  
180 185 190

Leu Ser Arg Ala Glu Glu Gly Tyr Glu Asn Leu Leu Ser Pro Ser Asp  
195 200 205

Met Thr His Ile Lys Ser Asp Thr Leu Ala Ser Lys His Ser Glu Leu  
210 215 220

Lys Asp Arg Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Lys  
225 230 235 240

Val Ser His Gln Gly Tyr Gly Pro Ala Thr Glu Phe Glu Glu Pro Arg  
245 250 255

Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Phe Thr Glu Lys  
260 265 270

Glu Leu Glu Ser Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile  
275 280 285

Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ser His Gln Lys  
290 295 300

Leu Lys His Val Glu Ser Ile Gly Asp Pro Glu His Ile Ser Arg Asn  
305 310 315 320

Lys Glu Lys Tyr Val Leu Leu Glu Glu Lys Thr Lys Glu Leu Gly Tyr  
325 330 335

Lys Val Lys Lys His Leu Gln Asp Leu Ser Ser Arg Val Ser Arg Ala  
340 345 350

Arg His Asn Glu Leu  
355

<210> 24  
<211> 348  
<212> PRT  
<213> Chicken

<400> 24

Met Gly Ala Thr Arg Thr Leu Val Ala Val Met Ala Ala Phe Leu Ala  
1 5 10 15

Val Ser Thr Arg Ala Ser Lys Tyr Thr Arg Glu Ala Asn Glu Gly Leu  
20 25 30

Ala Asp Ala Lys Arg Arg Glu Ala Gly Glu Phe Arg Val Val Arg Leu  
35 40 45

Asn Gln Val Trp Glu Lys Ala Gln Arg Leu Gln Leu Ser Ala Val Lys  
50 55 60

Leu Ala Glu Leu His Ser Asp Leu Lys Ile Gln Glu Lys Asp Glu Leu  
65 70 75 80

Ser Trp Lys Lys Leu Lys Ala Glu Gly Leu Gly Glu Asp Gly Glu Lys  
85 90 95

Glu Ala Lys Leu Arg Arg Asn Ile Asn Val Ile Met Thr Lys Tyr Gly  
100 105 110

Met Asn Gly Lys Lys Asp Ser His Leu Thr Asp Thr Asn Tyr Ile Lys  
115 120 125

Asp Gly Thr Glu Ser Asp Thr Leu Asp Asp Pro Arg Leu Glu Lys Leu  
130 135 140

Trp Ser Lys Ala Lys Thr Ser Gly Lys Phe Ser Asp Glu Glu Leu Asp  
145 150 155 160

Lys Leu Trp Arg Glu Phe Lys His His Lys Glu Lys Ile Arg Glu Tyr  
165 170 175

Asn Ile Leu Leu Glu Thr Val Ser Arg Thr Glu Asp Ile His Lys Lys  
180 185 190

Val Ile Asn Pro Ser Glu Glu Asn Pro Val Lys Glu Glu Val Leu His  
195 200 205

Asn Lys His Arg Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly  
210 215 220

Phe Glu Arg Leu Arg Lys Val Ser His Gln Gly Tyr Asp Ala Thr Ser  
225 230 235 240

Glu Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Met Ala Lys Ser  
245 250 255

Ala Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu Leu Lys  
260 265 270

His Phe Glu Ala Lys Ile Glu Lys His His His Tyr Gln Lys Gln Leu  
275 280 285

Glu Ile Ser His Glu Lys Leu Lys His Ile Glu Gly Thr Gly Asp Lys  
290 295 300

Glu His Leu Asn Arg Asn Arg Glu Lys Tyr Ala Met Leu Glu Glu Lys  
305 310 315 320

Thr Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp Leu Ser  
325 330 335

Ser Arg Ile Ser Gln Gly Leu Gln His Asn Glu Leu  
340 345

<210> 25  
<211> 331  
<212> PRT  
<213> Zebrafish

<400> 25

Met Ala Gly Lys Tyr Ser Lys Glu Met Asn Glu Lys Asn Ala Ser Asp  
1 5 10 15

Lys Ser Asn Asn Gln Val Glu Phe Arg Ile Ala Lys Leu Asn Gln Val  
20 25 30

Trp Glu Lys Ala Ile Arg Met Gln Leu Ala Pro Val Arg Leu Ser Glu  
35 40 45

Leu His Ser Asp Leu Lys Ile Gln Glu Lys Asp Glu Leu Gln Trp Lys  
50 55 60

Lys Leu Lys Ala Glu Gly Met Asp Glu Asp Gly Glu Arg Glu Ala Lys  
65 70 75 80

Leu Arg Arg Asn Phe Asn Ile Ile Leu Ala Lys Tyr Gly Met Asp Gly  
85 90 95

Lys Lys Asp Thr Arg Thr Leu Asp Ser Asn Arg Leu Lys Asp His Glu  
100 105 110

Val Lys Ile Gly Asp Thr Phe Asp Asp Pro Lys Leu Asp Lys Leu Trp  
115 120 125

Asn Lys Ala Arg Thr Ser Gly Lys Phe Ser Asp Glu Glu Leu Gln Thr  
130 135 140

Leu His Arg Glu Phe Gln His His Lys Asp Lys Ile His Glu Tyr Asn  
145 150 155 160

Ile Val Met Asp Thr Val Ser Arg Thr Glu Glu Ile His Lys Asn Val  
165 170 175

Ile Ser Pro Leu Glu Gly Asp Val Lys Glu Asn Val Leu His Gln Lys  
180 185 190

His Thr Asp Leu Lys Gln Arg Met Arg Asp Leu Asn Gln Gly Phe Glu  
195 200 205

Arg Leu Arg Lys Ile Thr His Glu Gly Tyr Thr Asp Asp Ser Glu Phe  
210 215 220

Arg Glu Pro Arg Val Ile Glu Leu Trp Glu Met Ala Lys Arg Ser Asn  
225 230 235 240

Leu Ser Glu Asp Glu Leu Asp Ser Leu Lys Glu Glu Leu Arg His Phe  
245 250 255

Glu Thr Lys Val Glu Lys His Gln His Tyr Gln Glu Gln Leu Glu Leu  
260 265 270

Ser His Gln Lys Leu Lys His Val Glu Ala Leu Gly Asp Glu Asp His  
275 280 285

Ile Met Arg Asn Lys Glu Lys Tyr Asn Thr Leu Ala Glu Lys Ala Arg  
290 295 300

Glu	Met	Gly	Tyr	Lys	Met	Lys	Lys	His	Leu	Gln	Asp	Leu	Thr	Asn	Lys
305					310					315					320
Leu Ser Lys Asn Gly Leu Gln His Asn Glu Leu															
					325				330						
<210> 26															
<211> 379															
<212> PRT															
<213> Fruit fly															
<400> 26															
Met Val Arg Ser Ala Leu Val Val Ala Ala Ile Ala Leu Ser Val Leu															
1				5				10				15			
Ile Ala Leu Gln Gly Val Asp Ala Asp Lys Lys Gln Ser Lys Lys Tyr															
				20				25				30			
Ser Lys Glu Ala Asn Asp Pro His Phe Gln Gln Val Lys Gln Glu Lys															
				35				40				45			
Tyr Asp Pro Asp Phe Lys Ser Ile Gln Arg Pro Phe Arg Met Ala Lys															
				50				55				60			
Leu Asn Leu Val Trp Ala Lys Ala Gln Asn Arg Leu Thr Glu Pro Lys															
				65				70				75			80
Leu Lys Ser Leu Tyr Met Glu Leu Lys Ile His Asp Lys Glu Glu Ile															
				85				90				95			
Ala Trp Lys Gln Leu Asn Ser Gln His Lys Asp Lys Asp Gly Leu Lys															
				100				105				110			
Ala Asp Glu Leu Arg Arg Lys Leu Ile Gly Ile Met Ser Ser Tyr Asp															
				115				120				125			
Leu Leu Glu His Phe Asp Asp Thr Gln Asp Thr Glu Lys Leu Lys Pro															
				130				135				140			
Tyr Lys Lys Phe His Asp Ala Glu Glu Arg His Arg Asn Lys Ser Leu															
				145				150				155			160
Phe Lys Asp Lys Lys Leu Asn Arg Leu Trp Glu Lys Ala Glu Ile Ser															
				165				170				175			
Gly Phe Thr Ala Glu Glu Leu Lys Ser Leu Lys Gln Glu Phe Asp His															
				180				185				190			

His Gln Asp Lys Val Asp Val Tyr Tyr Ser Leu Leu Glu Asn Ile Gly  
195 200 205

Thr Val Asp Thr Asp Lys His Glu Asn Ala Ile Asn Thr Glu Asp Leu  
210 215 220

Asp Thr Tyr Asn Leu Ile Ser Asn Asp Val Asn Glu Asn Asp Ile Lys  
225 230 235 240

Thr His Ala Gln Asn Val Lys Ser Phe Glu Asn Asp Leu Asn Thr Leu  
245 250 255

Arg Gly His His Thr Gly Ile Lys Asp His Tyr Asp Arg Leu Glu Arg  
260 265 270

Leu Val Ser Ser Gly Pro His Ser Gln Asp Phe Ile Glu Pro Lys Val  
275 280 285

Gln Gly Leu Trp Arg Val Ala Gln Ala Ser Asn Phe Thr Val Lys Glu  
290 295 300

Leu Glu Ser Ile Lys Thr Glu Leu His His Phe Glu Ser Arg Leu Leu  
305 310 315 320

Lys Leu Arg His Leu His Ala Glu His Ala Leu Gln Lys Glu Lys Tyr  
325 330 335

Lys Gly Glu Lys Val Lys Asp Lys Ser Ser Arg Phe Glu Glu Met Glu  
340 345 350

Asp Gln Leu Lys Lys Gln Thr Arg Lys Val Glu Lys Leu Gln Glu Asn  
355 360 365

Ile Glu Lys Thr Ile Phe Lys His Thr Glu Leu  
370 375

<210> 27  
<211> 400  
<212> PRT  
<213> Mosquito

<400> 27

Glu Leu Cys Pro Ile Ala Arg Arg Lys Arg Gly Ile Lys His Thr Leu  
1 5 10 15

Thr Met Pro Leu Phe Thr Arg Leu Cys Val Ile Val Phe Thr Val Leu  
20 25 30

Val Cys Asn His Val Val Gln Ser Glu Lys Ala His Ser Lys Tyr Ser  
35 40 45

Lys His Ala Asn Ala Leu Pro Asp Ser Glu Ile Tyr Glu Pro Asp Phe  
50 55 60

Arg Asn Ile Gln Arg Pro Phe Arg Met Ala Lys Leu Asn Leu Val Trp  
65 70 75 80

Thr Lys Ala Gln His Arg Leu Thr Glu Pro Lys Leu Lys Ser Leu Tyr  
85 90 95

Thr Glu Leu Lys Leu His Asp Lys Glu Glu Leu Thr Tyr Lys Gln Leu  
100 105 110

Lys Glu Lys Asp Lys Asp Gly Leu Lys Glu Ala Glu Leu Arg Asn Lys  
115 120 125

Leu Val Ser Ile Met Ser Thr Tyr Gly Leu Leu Glu His Phe Asp Asp  
130 135 140

Thr Gln Asp Pro Glu Lys Tyr Lys Leu Ala Lys Ser Ser Asp Gly Ala  
145 150 155 160

Pro Lys Lys Asp Thr Tyr Lys Asn Lys Ser Leu Phe Lys Asp Lys Lys  
165 170 175

Leu Asn Lys Leu Trp Asp Lys Ala Glu Ser Ala Gly Phe Thr Lys Glu  
180 185 190

Glu Leu Asp Ala Leu Arg Glu Glu Phe Asp His His Gln Ala Lys Ile  
195 200 205

Asp Val Tyr Tyr Ser Leu Leu Glu Arg Leu Gly Asp Asp Asp Asp Gly  
210 215 220

Gly Ala Ala Gly Gln Gly Ser Arg Arg Asp Asp Asp Ala Leu Leu Asn  
225 230 235 240

Ala Val Asn Asp Glu Glu His Asp Arg Tyr Asn Glu Val Asp Arg Ala  
245 250 255

Glu Glu Thr Asp Arg Ser Gln Pro Gly Ala Asn Lys Gln His Ala Tyr  
260 265 270

Leu His Lys Ser Asn Gln Leu Arg Glu Lys His Arg Glu Ile Arg Asp  
275 280 285

Asn Phe Asp Arg Leu Asp Arg Ile Ala Ser Lys Gly Pro Lys Ser Gln  
290 295 300

Asp Phe Val Glu Pro Lys Val Gln Gly Leu Trp Arg Val Ala Leu Ala  
305 310 315 320

Ser Asp Phe Ser Ala Asp Glu Leu Ala Ser Leu Lys Val Glu Leu Leu  
325 330 335

His Tyr Glu Ser Arg Leu Leu Lys Leu Arg His Met His Ala Glu His  
340 345 350

Ala Leu Ser Leu Glu Lys His Lys His Ser Asp Ala Lys Ala Asp Thr  
355 360 365

His Lys Leu Met Glu Asp Asn Ile Lys Lys Gln Thr Arg Lys Val Glu  
370 375 380

Lys Met Gln Glu Glu Val Glu Arg Arg Ile Phe Lys His Ser Glu Leu  
385 390 395 400

<210> 28  
<211> 331  
<212> PRT  
<213> Flatworm

<400> 28

Met Arg Asn His Phe Ser Phe Leu Leu Phe Leu Leu Val Ile Gly Ser  
1 5 10 15

Ala His Asn Lys Lys Thr Gln Tyr Arg Thr Glu Arg Ile Asn Phe Ile  
20 25 30

Tyr Glu Lys Ala Leu Gln His Val Thr Asp Arg Gln Asn Leu Ala Arg  
35 40 45

Leu Glu Lys Glu Leu Ser Gly Tyr Asp Ala Ile Tyr Leu Ala Ser Lys  
50 55 60

Ser Asn Arg Gln Gly Thr Gln Gly Thr Lys Glu Ile Asp Lys Ile Asp  
65 70 75 80

Asp Lys Leu Gly Lys Ile Leu Glu Lys Tyr Gly Leu Glu Lys Ala Val  
85 90 95

Leu Ala Phe Lys Glu Lys Tyr Lys His Lys Asn Leu Phe Gln Gln Thr  
100 105 110

Asp Asp Asn Glu Pro Leu Pro Ser Gly Lys Phe Thr Asp Gln Asn Leu  
115 120 125

Gln Lys Leu Trp Ser Gln Ala Gln Asn Gly Lys Phe Ser Gln Lys Glu  
130 135 140

Leu Asn Ala Leu His Gly Glu Leu Lys Glu Val Glu Gln Lys Met Arg  
145 150 155 160

Val Tyr Glu Asp Gln Leu Asp Asp Phe Lys Lys Val Pro His Glu Asn  
165 170 175

Ser Ile Gln His Asp Ile Glu Ser Ile Gly Asp Lys Thr Lys Lys Leu  
180 185 190

Lys Ala Ala Asn Arg Glu Leu Asn Asp His Leu Asp Glu Val His Arg  
195 200 205

Lys Val Thr Ser Glu Glu Phe Ser Pro Phe Asn Glu Pro Arg Val Lys  
210 215 220

Arg Leu Trp Lys Leu Ala Gln Glu Asn Glu Lys Leu Thr Pro His Glu  
225 230 235 240

Leu Ser Val Leu Lys Asp Glu Leu Ser His Phe Glu Ser Gln Leu Lys  
245 250 255

Lys Ile Glu Phe His Lys Val Phe Phe Phe Val Ala Asn Ser Cys Pro  
260 265 270

Lys Arg Gly Lys Asn Glu Glu Val Ser Arg Leu Gln Glu Asp Ala Glu  
275 280 285

Glu Arg Gly Lys Asp Lys Ser Gln Val Tyr Glu Asn Leu Glu Leu Ser  
290 295 300

Ile Lys His Glu Lys Leu Asn Arg Lys Ala Arg Lys Leu Glu Lys Tyr  
305 310 315 320

Ile Glu Glu Lys Ile Ile Ile His Arg Glu Leu  
325 330

<210> 29  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Synthetic peptide

<400> 29

Ala Glu Ala Glu Thr Gly  
1 5